

## SEQUENCE LISTING

&lt;110&gt; Chen, Lieping

&lt;120&gt; B7-H1, A NOVEL IMMUNOREGULATORY MOLECULE

&lt;130&gt; 07039/187001

&lt;140&gt; US 09/451,291

&lt;141&gt; 1999-11-30

&lt;160&gt; 12

&lt;170&gt; FastSEQ for Windows Version 4.0

&lt;210&gt; 1

&lt;211&gt; 290

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 1

Met Arg Ile Phe Ala Val Phe Ile Phe Met Thr Tyr Trp His Leu Leu  
 1 5 10 15  
 Asn Ala Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr  
 20 25 30  
 Gly Ser Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu  
 35 40 45  
 Asp Leu Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile  
 50 55 60  
 Ile Gln Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser  
 65 70 75 80  
 Tyr Arg Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn  
 85 90 95  
 Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr  
 100 105 110  
 Arg Cys Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val  
 115 120 125  
 Lys Val Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val  
 130 135 140  
 Asp Pro Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr  
 145 150 155 160  
 Pro Lys Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser  
 165 170 175  
 Gly Lys Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn  
 180 185 190  
 Val Thr Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr  
 195 200 205  
 Cys Thr Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu  
 210 215 220  
 Val Ile Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr His  
 225 230 235 240  
 Leu Val Ile Leu Gly Ala Ile Leu Leu Cys Leu Gly Val Ala Leu Thr  
 245 250 255  
 Phe Ile Phe Arg Leu Arg Lys Gly Arg Met Met Asp Val Lys Lys Cys  
 260 265 270  
 Gly Ile Gln Asp Thr Asn Ser Lys Lys Gln Ser Asp Thr His Leu Glu  
 275 280 285  
 Glu Thr  
 290



<210> 2  
 <211> 870  
 <212> DNA  
 <213> Homo sapiens

<400> 2  
 atgaggatat ttgctgtctt tatattcatg acctactggc atttgctgaa cgcatttact 60  
 gtcacgggttc ccaaggacct atatgtggta gagtatggta gcaatatgac aattgaatgc 120  
 aaattcccag tagaaaaaca attagacctg gctgcactaa ttgtctattg ggaaatggag 180  
 gataagaaca ttattcaatt tgtgcatgga gaggaagacc tgaagggttca gcatagtagc 240  
 tacagacaga gggcccggtt gttgaaggac cagctctccc tgggaaatgc tgcacttcag 300  
 atcacagatg tgaaattgca ggatgcaggg gtgtaccgct gcatgatcag ctatggtggt 360  
 gccgactaca agcgaattac tgtgaaagtc aatgccccat acaacaaaat caaccaaaga 420  
 attttgggtt tggatccagt cacctctgaa catgaactga catgtcaggc tgaggggtac 480  
 cccaaggccg aagtcactct gacaagcagt gaccatcaag tcctgagtgg taagaccacc 540  
 accaccaatt ccaagagaga ggagaagctt ttcaatgtga ccagcacact gagaatcaac 600  
 acaacaacta atgagatttt ctactgcact tttaggagat tagatcctga ggaaaaccat 660  
 acagctgaat tggatcatccc agaactacct ctggcacatc ctccaaatga aaggactcac 720  
 ttggttaattc tgggagccat cttattatgc cttggtgtag cactgacatt catcttccgt 780  
 ttaagaaaaa ggagaatgat ggatgtgaaa aaatgtggca tccaagatac aaactcaaag 840  
 aagcaaagtg atacacattt ggaggagacg 870

<210> 3  
 <211> 290  
 <212> PRT  
 <213> Mus musculus

<400> 3  
 Met Arg Ile Phe Ala Gly Ile Ile Phe Thr Ala Cys Cys His Leu Leu  
 1 5 10 15  
 Arg Ala Phe Thr Ile Thr Ala Pro Lys Asp Leu Tyr Val Val Glu Tyr  
 20 25 30  
 Gly Ser Asn Val Thr Met Glu Cys Arg Phe Pro Val Glu Arg Glu Leu  
 35 40 45  
 Asp Leu Leu Ala Leu Val Val Tyr Trp Glu Lys Glu Asp Glu Gln Val  
 50 55 60  
 Ile Gln Phe Val Ala Gly Glu Glu Asp Leu Lys Pro Gln His Ser Asn  
 65 70 75 80  
 Phe Arg Gly Arg Ala Ser Leu Pro Lys Asp Gln Leu Leu Lys Gly Asn  
 85 90 95  
 Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr  
 100 105 110  
 Cys Cys Ile Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Leu  
 115 120 125  
 Lys Val Asn Ala Pro Tyr Arg Lys Ile Asn Gln Arg Ile Ser Val Asp  
 130 135 140  
 Pro Ala Thr Ser Glu His Glu Leu Ile Cys Gln Ala Glu Gly Tyr Pro  
 145 150 155 160  
 Glu Ala Glu Val Ile Trp Thr Asn Ser Asp His Gln Pro Val Ser Gly  
 165 170 175  
 Lys Arg Ser Val Thr Thr Ser Arg Thr Glu Gly Met Leu Leu Asn Val  
 180 185 190  
 Thr Ser Ser Leu Arg Val Asn Ala Thr Ala Asn Asp Val Phe Tyr Cys  
 195 200 205  
 Thr Phe Trp Arg Ser Gln Pro Gly Gln Asn His Thr Ala Glu Leu Ile  
 210 215 220  
 Ile Pro Glu Leu Pro Ala Thr His Pro Pro Gln Asn Arg Thr His Trp  
 225 230 235 240  
 Val Leu Leu Gly Ser Ile Leu Leu Phe Leu Ile Val Val Ser Thr Val  
 245 250 255  
 Leu Leu Phe Leu Arg Lys Gln Val Arg Met Leu Asp Val Glu Lys Cys  
 260 265 270

Gly Val Glu Asp Thr Ser Ser Lys Asn Arg Asn Asp Thr Gln Phe Glu  
 275 280 285  
 Glu Thr  
 290

<210> 4  
 <211> 873  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (1)...(870)

<400> 4  
 atg agg ata ttt gct ggc att ata ttc aca gcc tgc tgt cac ttg cta 48  
 Met Arg Ile Phe Ala Gly Ile Ile Phe Thr Ala Cys Cys His Leu Leu  
 1 5 10 15  
 cgg gcg ttt act atc acg gct cca aag gac ttg tac gtg gtg gag tat 96  
 Arg Ala Phe Thr Ile Thr Ala Pro Lys Asp Leu Tyr Val Val Glu Tyr  
 20 25 30  
 ggc agc aac gtc acg atg gag tgc aga ttc cct gta gaa cgg gag ctg 144  
 Gly Ser Asn Val Thr Met Glu Cys Arg Phe Pro Val Glu Arg Glu Leu  
 35 40 45  
 gac ctg ctt gcg tta gtg gtg tac tgg gaa aag gaa gat gag caa gtg 192  
 Asp Leu Leu Ala Leu Val Val Tyr Trp Glu Lys Glu Asp Glu Gln Val  
 50 55 60  
 att cag ttt gtg gca gga gag gag gac ctt aag cct cag cac agc aac 240  
 Ile Gln Phe Val Ala Gly Glu Glu Asp Leu Lys Pro Gln His Ser Asn  
 65 70 75 80  
 ttc agg ggg aga gcc tcg ctg cca aag gac cag ctt ttg aag gga aat 288  
 Phe Arg Gly Arg Ala Ser Leu Pro Lys Asp Gln Leu Leu Lys Gly Asn  
 85 90 95  
 gct gcc ctt cag atc aca gac gtc aag ctg cag gac gca ggc gtt tac 336  
 Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr  
 100 105 110  
 tgc tgc ata atc agc tac ggt ggt gcg gac tac aag cga atc acg ctg 384  
 Cys Cys Ile Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Leu  
 115 120 125  
 aaa gtc aat gcc cca tac cgc aaa atc aac cag aga att tcc gtg gat 432  
 Lys Val Asn Ala Pro Tyr Arg Lys Ile Asn Gln Arg Ile Ser Val Asp  
 130 135 140  
 cca gcc act tct gag cat gaa cta ata tgt cag gcc gag ggt tat cca 480  
 Pro Ala Thr Ser Glu His Glu Leu Ile Cys Gln Ala Glu Gly Tyr Pro  
 145 150 155 160  
 gaa gct gag gta atc tgg aca aac agt gac cac caa ccc gtg agt ggg 528  
 Glu Ala Glu Val Ile Trp Thr Asn Ser Asp His Gln Pro Val Ser Gly  
 165 170 175  
 aag aga agt gtc acc act tcc cgg aca gag ggg atg ctt ctc aat gtg 576  
 Lys Arg Ser Val Thr Thr Ser Arg Thr Glu Gly Met Leu Leu Asn Val  
 180 185 190

acc agc agt ctg agg gtc aac gcc aca gcg aat gat gtt ttc tac tgt 624  
 Thr Ser Ser Leu Arg Val Asn Ala Thr Ala Asn Asp Val Phe Tyr Cys  
 195 200 205

acg ttt tgg aga tca cag cca ggg caa aac cac aca gcg gag ctg atc 672  
 Thr Phe Trp Arg Ser Gln Pro Gly Gln Asn His Thr Ala Glu Leu Ile  
 210 215 220

atc cca gaa ctg cct gca aca cat cct cca cag aac agg act cac tgg 720  
 Ile Pro Glu Leu Pro Ala Thr His Pro Pro Gln Asn Arg Thr His Trp  
 225 230 235 240

gtg ctt ctg gga tcc atc ctg ttg ttc ctc att gta gtg tcc acg gtc 768  
 Val Leu Leu Gly Ser Ile Leu Leu Phe Leu Ile Val Val Ser Thr Val  
 245 250 255

ctc ctc ttc ttg aga aaa caa gtg aga atg cta gat gtg gag aaa tgt 816  
 Leu Leu Phe Leu Arg Lys Gln Val Arg Met Leu Asp Val Glu Lys Cys  
 260 265 270

ggc gtt gaa gat aca agc tca aaa aac cga aat gat aca caa ttc gag 864  
 Gly Val Glu Asp Thr Ser Ser Lys Asn Arg Asn Asp Thr Gln Phe Glu  
 275 280 285

gag acg taa 873  
 Glu Thr  
 290

<210> 5  
 <211> 3616  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (73)...(942)

<400> 5  
 cccacgcgtc cgcagcttcc cgaggctccg caccagccgc gcttctgtcc gcctgcaggg 60  
 cattccagaa ag atg agg ata ttt gct gtc ttt ata ttc atg acc tac tgg 111  
 Met Arg Ile Phe Ala Val Phe Ile Phe Met Thr Tyr Trp  
 1 5 10

cat ttg ctg aac gca ttt act gtc acg gtt ccc aag gac cta tat gtg 159  
 His Leu Leu Asn Ala Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val  
 15 20 25

gta gag tat ggt agc aat atg aca att gaa tgc aaa ttc cca gta gaa 207  
 Val Glu Tyr Gly Ser Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu  
 30 35 40 45

aaa caa tta gac ctg gct gca cta att gtc tat tgg gaa atg gag gat 255  
 Lys Gln Leu Asp Leu Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp  
 50 55 60

aag aac att att caa ttt gtg cat gga gag gaa gac ctg aag gtt cag 303  
 Lys Asn Ile Ile Gln Phe Val His Gly Glu Glu Asp Leu Lys Val Gln  
 65 70 75

cat agt agc tac aga cag agg gcc cgg ctg ttg aag gac cag ctc tcc 351  
His Ser Ser Tyr Arg Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser  
80 85 90

ctg gga aat gct gca ctt cag atc aca gat gtg aaa ttg cag gat gca 399  
Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala  
95 100 105

ggg gtg tac cgc tgc atg atc agc tat ggt ggt gcc gac tac aag cga 447  
Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg  
110 115 120 125

att act gtg aaa gtc aat gcc cca tac aac aaa atc aac caa aga att 495  
Ile Thr Val Lys Val Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile  
130 135 140

ttg gtt gtg gat cca gtc acc tct gaa cat gaa ctg aca tgt cag gct 543  
Leu Val Val Asp Pro Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala  
145 150 155

gag ggc tac ccc aag gcc gaa gtc atc tgg aca agc agt gac cat caa 591  
Glu Gly Tyr Pro Lys Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln  
160 165 170

gtc ctg agt ggt aag acc acc acc acc aat tcc aag aga gag gag aag 639  
Val Leu Ser Gly Lys Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys  
175 180 185

ctt ttc aat gtg acc agc aca ctg aga atc aac aca aca act aat gag 687  
Leu Phe Asn Val Thr Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu  
190 195 200 205

att ttc tac tgc act ttt agg aga tta gat cct gag gaa aac cat aca 735  
Ile Phe Tyr Cys Thr Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr  
210 215 220

gct gaa ttg gtc atc cca gaa cta cct ctg gca cat cct cca aat gaa 783  
Ala Glu Leu Val Ile Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu  
225 230 235

agg act cac ttg gta att ctg gga gcc atc tta tta tgc ctt ggt gta 831  
Arg Thr His Leu Val Ile Leu Gly Ala Ile Leu Leu Cys Leu Gly Val  
240 245 250

gca ctg aca ttc atc ttc cgt tta aga aaa ggg aga atg atg gat gtg 879  
Ala Leu Thr Phe Ile Phe Arg Leu Arg Lys Gly Arg Met Met Asp Val  
255 260 265

aaa aaa tgt ggc atc caa gat aca aac tca aag aag caa agt gat aca 927  
Lys Lys Cys Gly Ile Gln Asp Thr Asn Ser Lys Lys Gln Ser Asp Thr  
270 275 280 285

cat ttg gag gag acg taatccagca ttggaacttc tgatcttcaa gcagggattc 982  
His Leu Glu Glu Thr  
290

tcaacctgtg gtttaggggt tcatcggggc tgagcgtgac aagaggaagg aatggacccg 1042  
tgggatgcag gcaatgtggg acttaaaagg cccaagcact gaaaatggaa cctggcgaaa 1102  
gcagaggagg agaatgaaga aagatggagt caaacaggga gcctggaggg agaccttgat 1162  
actttcaaag gcctgagggg ctcacgcagc cctgtgacag ggagaaaagga tactttctgaa 1222  
caaggagcct ccaagcaaat catccattgc tcatcctagg aagacgggtt gagaatccct 1282  
aatttgaggg tcagttcctg cagaagtgcc ctttgccctc actcaatgcc tcaatttctt 1342

ttctgcatga ctgagagtct cagtgttggga acgggacagt atttatgtat gagtttttcc 1402  
 tatttatttt gagtctgtga ggtcttcttg tcatgtgagt gtggttgtga atgatttctt 1462  
 ttgaagatat attgtagtag atgttacaat tttgtcgcca aactaaactt gctgcttaat 1522  
 gatttgctca catctagtaa aacatggagt atttgtaagg tgcttgggtct cctctataac 1582  
 tacaagtata cattggaagc ataaagatca aaccgttggg tgcataggat gtcaccttta 1642  
 ttttaacccat taatactctg gttgacctaa tcttattctc agacctcaag tgtctgtgca 1702  
 gtatctgttc catttaaata tcagctttac aattatgtgg tagcctacac acataatctc 1762  
 atttcatcgc tgtaaccacc ctgttgtgat aaccactatt attttaccba tcgtacagct 1822  
 gaggaagcaa acagattaag taacttgccc aaaccagtaa atagcagacc tcagactgcc 1882  
 acccactgtc cttttataat acaatttaca gctatatattt actttaagca attcttttat 1942  
 tcaaaaacca tttattaagt gcccttgcaa tatcaatcgc tgtgccaggc attgaatcta 2002  
 cagatgtgag caagacaaaag tacctgtcct caaggagctc atagtataat gaggagatta 2062  
 acaagaaaat gtattattac aatttagtcc agtgtcatag cataaggatg atgagagggg 2122  
 aaaacccgag cagtgttgcc aagaggagga aataggccaa tgtggtctgg gacggttggg 2182  
 tatacttaaa catcttaata atcagagtaa tttctattta caaagagagg tcggtactta 2242  
 aaataaccct gaaaaataac actggaattc cttttctagc attatattta ttcttgattt 2302  
 gcctttgcca tataatctaa tgcttgttta tatagtgtct ggtattgttt aacagttctg 2362  
 tcttttctat ttaaatgcca ctaaaatttt aattcatacc tttccatgat tcaaaattca 2422  
 aaagatccca tgggagatgg ttggaaaatc tccacttcat cctccaagcc attcaagttt 2482  
 cctttccaga agcaactgct actgcctttc attcatatgt tcttctaaag atagtctaca 2542  
 tttggaaatg tatgttaaaa gcacgtattt ttaaaatttt tttcctaaat agtaacacat 2602  
 tgtatgtctg ctgtgtactt tgctattttt atttatttta gtgtttctta tatagcagat 2662  
 ggaatgaatt tgaagttccc agggctgagg atccatgcct tctttgtttc taagttatct 2722  
 ttcccatagc ttttcattat ctttcatatg atccagtata tgtaaataat gtcctacata 2782  
 tacattttaga caaccaccat ttgttaagta tttgctctag gacagagttt ggatttgttt 2842  
 atgtttgctc aaaaggagac ccattgggctc tccagggtgc actgagtcaa tctagtctca 2902  
 aaaagcaatc ttattattaa ctctgtatga cagaatcatg tctggaactt ttgttttctg 2962  
 ctttctgtca agtataaact tcactttgat gctgtacttg caaaatcaca ttttctttct 3022  
 ggaaattccg gcagtgtacc ttgactgcta gctaccctgt gccagaaaag cctcattcgt 3082  
 tgtgcttgaa cccttgaatg ccaccagctg tcatcactac acagccctcc taagaggctt 3142  
 cctggaggtt tcgagattca gatgccctgg gagatcccag agtttctttt cctctttggc 3202  
 catattctgg tgtcaatgac aaggagtacc ttggctttgc cacatgtcaa ggctgaagaa 3262  
 acagtgtctc caacagagct ccttgtgtta tctgtttgta catgtgcatt tgtacagtaa 3322  
 ttggtgtgac agtgttcttt gtgtgaatta caggcaagaa ttgtggctga gcaaggcaca 3382  
 tagtctactc agtctattcc taagtccctaa ctctccttg tggtgttggg tttgtaaggc 3442  
 actttatccc ttttgtctca tgtttcatcg taaatggcat aggcagagat gatacctaatt 3502  
 tctgcatttg attgtcactt tttgtacctg cattaattta ataaaatatt cttattttatt 3562  
 ttgttacttg gtaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 3616

<210> 6  
 <211> 25  
 <212> PRT  
 <213> Homo sapiens

<400> 6  
 Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val  
 1 5 10 15  
 Leu Met Ser Ala Gln Glu Ser Trp Ala  
 20 25

<210> 7  
 <211> 5  
 <212> PRT  
 <213> Bovidae

<400> 7  
 Lys Phe Glu Arg Gln  
 1 5

<210> 8  
 <211> 15

<212> PRT  
 <213> Homo sapiens

<400> 8  
 Met Asp Asp Gln Arg Asp Leu Ile Ser Asn Asn Glu Gln Leu Pro  
           1                  5                  10                  15

<210> 9  
 <211> 4  
 <212> PRT  
 <213> Rattus rattus

<400> 9  
 Lys Asp Glu Leu  
           1

<210> 10  
 <211> 210  
 <212> PRT  
 <213> Homo sapiens

<400> 10  
 Val Glu Tyr Gly Ser Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu  
           1                  5                  10                  15  
 Lys Gln Leu Asp Leu Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp  
                   20                  25                  30  
 Lys Asn Ile Ile Gln Phe Val His Gly Glu Glu Asp Leu Lys Val Gln  
                   35                  40                  45  
 His Ser Ser Tyr Arg Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser  
           50                  55                  60  
 Leu Gly Asn Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala  
           65                  70                  75                  80  
 Gly Val Tyr Arg Cys Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg  
                   85                  90                  95  
 Ile Thr Val Lys Val Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile  
                   100                  105                  110  
 Leu Val Val Asp Pro Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala  
           115                  120                  125  
 Glu Gly Tyr Pro Lys Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln  
           130                  135                  140  
 Val Leu Ser Gly Lys Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys  
           145                  150                  155                  160  
 Leu Phe Asn Val Thr Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu  
                   165                  170                  175  
 Ile Phe Tyr Cys Thr Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr  
                   180                  185                  190  
 Ala Glu Leu Val Ile Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu  
           195                  200                  205  
 Arg Thr  
           210

<210> 11  
 <211> 205  
 <212> PRT  
 <213> Homo sapiens

<400> 11  
 Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys Gly His Asn Val Ser  
           1                  5                  10                  15  
 Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp Gln Lys Glu Lys Lys  
                   20                  25                  30

Met Val Leu Thr Met Met Ser Gly Asp Met Asn Ile Trp Pro Glu Tyr  
           35                  40                  45  
 Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn Leu Ser Ile Val Ile  
       50                  55                  60  
 Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr Glu Cys Val Val Leu  
       65                  70                  75                  80  
 Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His Leu Ala Glu Val Thr  
                   85                  90                  95  
 Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser Ile Ser Asp Phe Glu  
                   100                  105                  110  
 Ile Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys Ser Thr Ser Gly Gly  
                   115                  120                  125  
 Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn Gly Glu Glu Leu Asn  
       130                  135                  140  
 Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu Thr Glu Leu Tyr Ala  
       145                  150                  155                  160  
 Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr Asn His Ser Phe Met  
                   165                  170                  175  
 Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn Gln Thr Phe Asn Trp  
                   180                  185                  190  
 Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn Leu Leu  
                   195                  200                  205

<210> 12  
 <211> 218  
 <212> PRT  
 <213> Homo sapiens

<400> 12  
 Ala Tyr Phe Asn Glu Thr Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser  
       1                  5                  10                  15  
 Gln Asn Gln Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Glu  
                   20                  25                  30  
 Asn Leu Val Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser  
                   35                  40                  45  
 Val His Ser Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp  
       50                  55                  60  
 Thr Leu Arg Leu His Asn Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln  
       65                  70                  75                  80  
 Cys Ile Ile His His Lys Lys Pro Thr Gly Met Ile Arg Ile His Gln  
                   85                  90                  95  
 Met Asn Ser Glu Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile  
                   100                  105                  110  
 Val Pro Ile Ser Asn Ile Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys  
                   115                  120                  125  
 Ser Ser Ile His Gly Tyr Pro Glu Pro Lys Lys Met Ser Val Leu Leu  
       130                  135                  140  
 Arg Thr Lys Asn Ser Thr Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser  
       145                  150                  155                  160  
 Gln Asp Asn Val Thr Glu Leu Tyr Asp Val Ser Ile Ser Leu Ser Val  
                   165                  170                  175  
 Ser Phe Pro Asp Val Thr Ser Asn Met Thr Ile Phe Cys Ile Leu Glu  
                   180                  185                  190  
 Thr Asp Lys Thr Arg Leu Leu Ser Pro Phe Ser Ile Glu Leu Glu  
                   195                  200                  205  
 Asp Pro Gln Pro Pro Pro Asp His Ile Pro  
       210                  215